TI Mechanistic and genetic overlap of barley host and non-host resistance to Blumeria graminis.

L2 ANSWER 15 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI A single-amino acid substitution in the sixth leucine-rich repeat of barley MLA6 and MLA13 alleviates dependence on **RAR1** for disease resistance signaling.

L2 ANSWER 16 OF 80 CAPLUS COPYRIGHT 2005 ACS on STN
TI Functional analysis of proteins essential for plant disease resistance

L2 ANSWER 17 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Maize **Rar1** polynucleotides and methods of use.

L2 ANSWER 18 OF 80 CAPLUS COPYRIGHT 2005 ACS on STN
TI Protein and cDNA sequences of rice disease resistance protein **RAR1** and uses for disease resistant transgenic plants

L2 ANSWER 19 OF 80 CAPLUS COPYRIGHT 2005 ACS on STN
TI cDNAs encoding corn **Rar1**-interactor proteins and their use in improving transgenic plant disease resistance

L2 ANSWER 20 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI HSP90 interacts with **RAR1** and SGT1 and is essential for RPS2-mediated disease resistance in Arabidopsis.

L2 ANSWER 21 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Cytosolic HSP90 associates with and modulates the Arabidopsis RPM1 disease resistance protein.

L2 ANSWER 22 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Role of SGT1 in the regulation of plant R gene signalling.

L2 ANSWER 23 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Two MAPK cascades, NPR1, and TGA transcription factors play a role in Pto-mediated disease resistance in tomato.

L2 ANSWER 24 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Recognition specificity and **RAR1**/SGT1 dependence in barley Mla disease resistance genes to the powdery mildew fungus.

L2 ANSWER 25 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Powdery mildew-induced Mla mRNAs are alternatively spliced and contain multiple upstream open reading frames.

=> d bib abs 20 21 22 15 7 8 10

L2 ANSWER 20 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2003:575011 BIOSIS
DN PREV200300580244
TI HSP90 interacts with **RAR1** and SGT1 and is essential for RPS2-mediated disease resistance in Arabidopsis.
AU Takahashi, Akira; Casais, Catarina; Ichimura, Kazuya; Shirasu, Ken [Reprint Author]
CS John Innes Centre, The Sainsbury Laboratory, Colney Lane, Norwich, NR4 7UH, UK
ken.shirasu@sainsbury-laboratory.ac.uk
SO Proceedings of the National Academy of Sciences of the United States of America, (September 30 2003) Vol. 100, No. 20, pp. 11777-11782. print.
ISSN: 0027-8424 (ISSN print).
DT Article
LA English
ED Entered STN: 10 Dec 2003
Last Updated on STN: 10 Dec 2003
AB **RAR1** and its interacting partner SGT1 play a central role in plant disease resistance triggered by a number of resistance (R) proteins.

We identified cytosolic heat shock protein 90 (HSP90), a molecular chaperone, as another **RAR1** interacting protein by yeast two-hybrid screening. **RAR1** interacts with the N-terminal half of HSP90 that contains the ATPase domain. HSP90 also specifically interacts with SGT1 that contains a tetratricopeptide repeat motif and a domain with similarity to the cochaperone p23. In Arabidopsis, the HSP90 inhibitor geldanamycin reduces the hypersensitive response and abolishes resistance triggered by the R protein RPS2 against Pseudomonas syringae pv. tomato DC3000 (avrRpt2). One of four Arabidopsis cytosolic HSP90 isoforms, AtHSP90.1 is required for full RPS2 resistance and is rapidly induced upon pathogen challenge. We propose that **RAR1** and SGT1 function closely with HSP90 in chaperoning roles that are essential for disease resistance.

L2 ANSWER 21 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2004:43056 BIOSIS
DN PREV200400044089
TI Cytosolic HSP90 associates with and modulates the Arabidopsis RPM1 disease resistance protein.
AU Hubert, David A.; Tornero, Pablo; Belkhadir, Youssef; Krishna, Priti; Takahashi, Akira; Shirasu, Ken; Dangl, Jeffery L. [Reprint Author]
CS Department of Biology, University of North Carolina at Chapel Hill, Coker Hall, Room 108, CB 3280, Chapel Hill, NC, 27599, USA
dangl@email.unc.edu
SO EMBO (European Molecular Biology Organization) Journal, (November 3 2003) Vol. 22, No. 21, pp. 5679-5689. print.
ISSN: 0261-4189 (ISSN print).
DT Article
LA English
ED Entered STN: 14 Jan 2004
Last Updated on STN: 14 Jan 2004
AB The Arabidopsis protein RPM1 activates disease resistance in response to Pseudomonas syringae proteins targeted to the inside of the host cell via the bacterial type III delivery system. We demonstrate that specific mutations in the ATP-binding domain of a single Arabidopsis cytosolic HSP90 isoform compromise RPM1 function. These mutations do not affect the function of related disease resistance proteins. RPM1 associates with HSP90 in plant cells. The Arabidopsis proteins **RAR1** and SGT1 are required for the action of many R proteins, and display some structural similarity to HSP90 co-chaperones. Each associates with HSP90 in plant cells. Our data suggest that (i) RPM1 is an HSP90 client protein; and (ii) **RAR1** and SGT1 may function independently as HSP90 cofactors. Dynamic interactions among these proteins can regulate RPM1 stability and function, perhaps similarly to the formation and regulation of animal steroid receptor complexes.

L2 ANSWER 22 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2004:10271 BIOSIS
DN PREV200400012573
TI Role of SGT1 in the regulation of plant R gene signalling.
AU Muskett, Paul; Parker, Jane [Reprint Author]
CS Department of Plant-Microbe Interactions, Max-Planck Institute for Plant Breeding Research, Carl-von-Linne-Weg 10, 50829, Cologne, Germany
parker@mpiz-koeln.mpg.de
SO Microbes and Infection, (September 2003) Vol. 5, No. 11, pp. 969-976. print.
ISSN: 1286-4579.
DT Article
LA English
ED Entered STN: 24 Dec 2003
Last Updated on STN: 24 Dec 2003
AB Recent important discoveries in several laboratories have identified SGT1 as an essential component of R gene-mediated disease resistance in plants. The precise molecular function of SGT1 remains unknown, although sequence analysis and structural predictions reveal that SGT1 has features of co-chaperones that associate with HSP90 in animals. This review will describe the role of SGT1 in R gene-mediated plant defence and discuss how

SGT1 may regulate this process.

L2 ANSWER 15 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2004:266135 BIOSIS
DN PREV200400265071
TI A single-amino acid substitution in the sixth leucine-rich repeat of barley MLA6 and MLA13 alleviates dependence on **RAR1** for disease resistance signaling.
AU Halterman, Dennis A.; Wise, Roger P. [Reprint Author]
CS USDA ARSDept Plant Pathol, Iowa State Univ, Ames, IA, 50011, USA
rpwise@iastate.edu
SO Plant Journal, (April 2004) Vol. 38, No. 2, pp. 215-226. print.
ISSN: 0960-7412 (ISSN print).
DT Article
LA English
ED Entered STN: 26 May 2004
Last Updated on STN: 26 May 2004
AB Interactions between barley and the powdery mildew pathogen, Blumeria graminis f. sp. hordei, (Bgh) are determined by unique combinations of host resistance genes, designated Mildew-resistance locus (Ml), and cognate pathogen avirulence genes. These interactions occur both dependent and independent of **Rar1** (required for Mla12 resistance) and Sgt1 (Suppressor of G-two allele of skp1), which are differentially required for diverse plant disease-resistance pathways. We have isolated two new functional Mla alleles, **Rar1**-independent Mla7 and **Rar1**-dependent Mla10, as well as the Mla paralogs, Mla6-2 and Mla13-2. Utilizing the inherent diversity amongst Mla-encoded proteins, we identified the only two amino acids exclusively conserved in **RAR1**-dependent MLA6, MLA10, MLA12, and MLA13 that differ at the corresponding position in **RAR1**-independent MLA1 and MLA7. Two- and three-dimensional modeling places these residues on a predicted surface of the sixth leucine-rich repeat (LRR) domain at positions distinct from those within the beta-sheets hypothesized to determine resistance specificity. Site-directed mutagenesis of these residues indicates that **RAR1** independence requires the presence of an aspartate at position 721, as mutation of this residue to a structurally similar, but uncharged, asparagine did not alter **RAR1** dependence. These results demonstrate that a single-amino acid substitution in the sixth MLA LRR can alter host signaling but not resistance specificity to B. graminis.

L2 ANSWER 7 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
AN 2005:120954 BIOSIS
DN PREV200500110915
TI **RAR1** positively controls steady state levels of barley MLA resistance proteins and enables sufficient MLA6 accumulation for effective resistance.
AU Bieri, Stphane [Reprint Author]; Mauch, Stefan; Shen, Qian-Hua; Peart, Jack; Devoto, Alessandra; Casais, Catarina; Ceron, Francesca; Schulze, Sabine; Steinbiss, Hans-Henning; Shirasu, Ken; Schulze-Lefert, Paul
CS Dept Plant Microbe Interact, Max Planck Inst Zuchtungsforsch, D-50829, Cologne, Germany
bieri@mpiz-koeln.mpg.de
SO Plant Cell, (December 2004) Vol. 16, No. 12, pp. 3480-3495. print.
CODEN: PLCEEW. ISSN: 1040-4651.
DT Article
LA English
ED Entered STN: 23 Mar 2005
Last Updated on STN: 23 Mar 2005
AB The polymorphic barley (Hordeum vulgare) Mla locus harbors allelic race-specific resistance (R) genes to the powdery mildew fungus Blumeria graminis f sp hordei. The highly sequence-related MLA proteins contain an N-terminal coiled-coil structure, a central nucleotide binding (NB) site, a Leu-rich repeat (LRR) region, and a C-terminal non-LRR region. Using transgenic barley lines expressing epitope-tagged MLA1 and MLA6 derivatives driven by native regulatory sequences, we show a reversible and salt concentration-dependent distribution of the intracellular MLA

proteins in soluble and membrane-associated pools. A posttranscriptional process directs fourfold greater accumulation of MLA1 over MLA6. Unexpectedly, in **rar1** mutant plants that are compromised for MLA6 but not MLA1 resistance, the steady state level of both MLA isoforms is reduced. Furthermore, differential steady state levels of MLA1/MLA6 hybrid proteins correlate with their requirement for **RAR1**; the **RAR1**-independent hybrid protein accumulates to higher levels and the **RAR1**-dependent one to lower levels. Interestingly, yeast two-hybrid studies reveal that the LRR domains of **RAR1** -independent but not **RAR1**-dependent MLA isoforms interact with SGT1, a **RAR1** interacting protein required for the function of many NB-LRR type R proteins. Our findings implicate the existence of a conserved mechanism to reach minimal NB-LRR R protein thresholds that are needed to trigger effective resistance responses.

L2 ANSWER 8 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
AN 2005:42423 BIOSIS
DN PREV200500041521
TI Arabidopsis RIN4 negatively regulates disease resistance mediated by RPS2 and RPM1 downstream or independent of the NDR1 signal modulator and is not required for the virulence functions of bacterial type III effectors AvrRpt2 or AvrRpm1.
AU Belkhadir, Youssef; Nimchuk, Zachary; Hubert, David A.; Mackey, David; Dangl, Jeffery L. [Reprint Author]
CS Dept Biol, Univ N Carolina, Chapel Hill, NC, 27599, USA
dangl@email.unc.edu
SO Plant Cell, (October 2004) Vol. 16, No. 10, pp. 2822-2835. print.
CODEN: PLCEEW. ISSN: 1040-4651.
DT Article
LA English
ED Entered STN: 26 Jan 2005
Last Updated on STN: 26 Jan 2005
AB Bacterial pathogens deliver type III effector proteins into the plant cell during infection. On susceptible (r) hosts, type III effectors can contribute to virulence. Some trigger the action of specific disease resistance (R) gene products. The activation of R proteins can occur indirectly via modification of a host target. Thus, at least some type III effectors are recognized at site(s) where they may act as virulence factors. These data indicate that a type III effector's host target might be required for both initiation of R function in resistant plants and pathogen virulence in susceptible plants. In Arabidopsis thaliana, RPM1-interacting protein 4 (RIN4) associates with both the Resistance to Pseudomonas syringae pv maculicola 1 (RPM1) and Resistance to P. syringae 2 (RPS2) disease resistance proteins. RIN4 is posttranslationally modified after delivery of the P. syringae type III effectors AvrRpm1, AvrB, or AvrRpt2 to plant cells. Thus, RIN4 may be a target for virulence functions of these type III effectors. We demonstrate that RIN4 is not the only host target for AvrRpm1 and AvrRpt2 in susceptible plants because its elimination does not diminish their virulence functions. In fact, RIN4 negatively regulates AvrRpt2 virulence function. RIN4 also negatively regulates inappropriate activation of both RPM1 and RPS2. Inappropriate activation of RPS2 is nonspecific disease resistance 1 (NDR1) independent, in contrast with the established requirement for NDR1 during AvrRpt2-dependent RPS2 activation. Thus, RIN4 acts either cooperatively, downstream, or independently of NDR1 to negatively regulate RPS2 in the absence of pathogen. We propose that many P. syringae type III effectors have more than one target in the host cell. We suggest that a limited set of these targets, perhaps only one, are associated with R proteins. Thus, whereas any pathogen virulence factor may have multiple targets, the perturbation of only one is necessary and sufficient for R activation.

L2 ANSWER 10 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2004:238682 BIOSIS
DN PREV200400239097
TI Molecular chaperone Hsp90 associates with resistance protein N and its signaling proteins SGT1 and **Rar1** to modulate an innate immune

response in plants.
AU Liu, Yule; Burch-Smith, Tessa; Schiff, Michael; Feng, Suhua; Dinesh-Kumar, Savithramma P. [Reprint Author]
CS Department of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, CT, 06520, USA
savithramma.dinesh-kumar@yale.edu
SO Journal of Biological Chemistry, (January 16 2004) Vol. 279, No. 3, pp. 2101-2108. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 6 May 2004
Last Updated on STN: 6 May 2004
AB SGT1 and **Rar1** are important signaling components of resistance (R) gene-mediated plant innate immune responses. Here we report that SGT1 and **Rar1** associate with the molecular chaperone Hsp90. In addition, we show that Hsp90 associates with the resistance protein N that confers resistance to tobacco mosaic virus. This suggests that Hsp90-SGT1-**Rar1** and R proteins might exist in one complex. Suppression of Hsp90 in Nicotiana benthamiana plants shows that it plays an important role in plant growth and development. In addition, Hsp90 suppression in NN plants compromises N-mediated resistance to tobacco mosaic virus. Our results reveal a new role for SGT1- and **Rar1** -associated chaperone machinery in R gene-mediated defense signaling.

=> d ti 26-35

L2 ANSWER 26 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Deciphering host resistance and pathogen virulence: The Arabidopsis/Pseudomonas interaction as a model.

L2 ANSWER 27 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI The role of proteolysis in R gene mediated defence in plants.

L2 ANSWER 28 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Complex formation, promiscuity and multi-functionality: Protein interactions in disease-resistance pathways.

L2 ANSWER 29 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI A single amino acid substitution in the sixth leucine-rich repeat of barley MLA alleviates dependence on **RAR1** for disease resistance signaling.

L2 ANSWER 30 OF 80 CAPLUS COPYRIGHT 2005 ACS on STN
TI Resistance gene signaling in plants - complex similarities to animal innate immunity

L2 ANSWER 31 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Regulatory role of SGT1 in early R gene-mediated plant defenses.

L2 ANSWER 32 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI The **RAR1** interactor SGT1, an essential component of R gene-triggered disease resistance.

L2 ANSWER 33 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Resisting attack.

L2 ANSWER 34 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Role of SCF ubiquitin-ligase and the COP9 signalosome in the N gene-mediated resistance response to Tobacco mosaic virus.

L2 ANSWER 35 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI **RAR1** and NDR1 contribute quantitatively to disease resistance in Arabidopsis, and their relative contributions are dependent on the R gene assayed.

=> d bib abs 32 31 27

L2 ANSWER 32 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2002:233031 BIOSIS
DN PREV200200233031
TI The **RAR1** interactor SGT1, an essential component of R gene-triggered disease resistance.
AU Azevedo, Cristina; Sadanandom, Ari; Kitagawa, Katsumi; Freialdenhoven, Andreas; Shirasu, Ken [Reprint author]; Schulze-Lefert, Paul
CS Sainsbury Laboratory, John Innes Centre, Colney Lane, Norwich, NR4 7UH, UK ken.shirasu@bbsrc.ac.uk
SO Science (Washington D C), (15 March, 2002) Vol. 295, No. 5562, pp. 2073-2076. print.
CODEN: SCIEAS. ISSN: 0036-8075.
DT Article
LA English
ED Entered STN: 10 Apr 2002
Last Updated on STN: 10 Apr 2002
AB Plant disease resistance (R) genes trigger innate immune responses upon pathogen attack. **RAR1** is an early convergence point in a signaling pathway engaged by multiple R genes. Here, we show that **RAR1** interacts with plant orthologs of the yeast protein SGT1, an essential regulator in the cell cycle. Silencing the barley gene Sgt1 reveals its role in R gene-triggered, **Rar1**-dependent disease resistance. SGT1 associates with SKP1 and CUL1, subunits of the SCF (Skp1-Cullin-F-box) ubiquitin ligase complex. Furthermore, the **RAR1**-SGT1 complex also interacts with two COP9 signalosome components. The interactions among **RAR1**, SGT1, SCF, and signalosome subunits indicate a link between disease resistance and ubiquitination.

L2 ANSWER 31 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2002:233032 BIOSIS
DN PREV200200233032
TI Regulatory role of SGT1 in early R gene-mediated plant defenses.
AU Austin, Mark J.; Muskett, Paul; Kahn, Katherine; Feys, Bart J.; Jones, Jonathan D. G.; Parker, Jane E. [Reprint author]
CS Sainsbury Laboratory, John Innes Centre, Colney Lane, Norwich, NR4 7UH, UK parker@mpiz-koeln.mpg.de
SO Science (Washington D C), (15 March, 2002) Vol. 295, No. 5562, pp. 2077-2080. print.
CODEN: SCIEAS. ISSN: 0036-8075.
DT Article
LA English
ED Entered STN: 10 Apr 2002
Last Updated on STN: 10 Apr 2002
AB Animal SGT1 is a component of Skp1-Cullin-F-box protein (SCF) ubiquitin ligases that target regulatory proteins for degradation. Mutations in one (SGT1b) of two highly homologous Arabidopsis SGT1 genes disable early plant defenses conferred by multiple resistance (R) genes. Loss of SGT1b function in resistance is not compensated for by SGT1a. R genes differ in their requirements for SGT1b and a second resistance signaling gene, **RAR1**, that was previously implicated as an SGT1 interactor. Moreover, SGT1b and **RAR1** contribute additively to RPP5-mediated pathogen recognition. These data imply both operationally distinct and cooperative functions of SGT1 and **RAR1** in plant disease resistance.

L2 ANSWER 27 OF 80 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2003:444786 BIOSIS
DN PREV200300444786
TI The role of proteolysis in R gene mediated defence in plants.
AU Tor, Mahmut [Reprint Author]; Yemm, Antony; Holub, Eric
CS Sustainable Disease Resistance Team, Horticulture Research International, Wellesbourne, Warwick, CV35 9EF, UK
Mahmut.tor@hri.ac.uk

SO Molecular Plant Pathology, (July 2003) Vol. 4, No. 4, pp. 287-296. print.
ISSN: 1464-6722 (ISSN print).
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 24 Sep 2003
Last Updated on STN: 24 Sep 2003
AB Within the last 10 years, numerous R genes have been cloned from natural genetic variation in model as well as crop plants, and these have been classified according to their motifs. Some of the downstream signalling components have also been identified by artificial mutagenesis. Recently, cloning of three of these signalling genes (COI1, **RAR1** and SGT1b) from Arabidopsis, barley and tobacco have helped uncover the physiological link between defence signalling and ubiquitin-mediated protein degradation. The physical association of COI1 and SGT1b with the components of ubiquitin-ligase complexes has been shown. In addition, post-transcriptional silencing of some of the subunits of the ubiquitin-ligase complex has led to a loss of resistance, indicating that protein degradation may also act as a regulatory mechanism in plant defence. Over the next few years, we should expect to see more examples of the interplay between the defence response and protein degradation in plants.

=> logoff hold
STN INTERNATIONAL SESSION SUSPENDED AT 16:12:55 ON 03 MAY 2005

FILE 'HOME' ENTERED AT 14:44:02 ON 05 MAY 2005

=> file biosis caplus caba agricola

=> s sgt1?
L1 168 SGT1?

=> duplicate remove l1L2 87 DUPLICATE REMOVE L1 (81 DUPLICATES REMOVED)

=> d ti 1-15

L2 ANSWER 1 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Molecular genetic evidence for the role of **SGT1** in the intramolecular complementation of Bs2 protein activity in Nicotiana benthamiana

L2 ANSWER 2 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI A systematic review of large scale and heterogeneous gene array data in heart failure

L2 ANSWER 3 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Mammalian CHORD-containing protein 1 is a novel heat shock protein 90-interacting protein.

L2 ANSWER 4 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Metabolic compensation of steroidal glycoalkaloid biosynthesis in transgenic potato tubers: using reverse genetics to confirm the in vivo enzyme function of a steroidal alkaloid galactosyltransferase.

L2 ANSWER 5 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Differences in intensity and specificity of hypersensitive response induction in Nicotiana spp. by INF1, INF2A, and INF2B of Phytophthora infestans

L2 ANSWER 6 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI The atypical resistance gene, RPW8, recruits components of basal defence for powdery mildew resistance in Arabidopsis

L2 ANSWER 7 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Cell proliferation-related polypeptides and encoding nucleic acids in rice and their uses for plant transformation

L2 ANSWER 8 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Rice genes induced by stress and their products and their use in the improvement of stress tolerance in crop plants

L2 ANSWER 9 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Human **Sgt1** binds HSP90 through the CHORD-**Sgt1** domain and not the tetratricopeptide repeat domain.

L2 ANSWER 10 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI The interaction between **Sgt1p** and Skp1p is regulated by HSP90 chaperones and is required for proper CBF3 assembly.

L2 ANSWER 11 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI **Sgt1** associates with Hsp90: an initial step of assembly of the core kinetochore complex.

L2 ANSWER 12 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI RAR1 positively controls steady state levels of barley MLA resistance proteins and enables sufficient MLA6 accumulation for effective resistance.

L2 ANSWER 13 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI **Sgt1p** and Skp1p modulate the assembly and turnover of CBF3 complexes required for proper kinetochore function.

L2 ANSWER 14 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Molecular chaperone Hsp90 associates with resistance protein N and its signaling proteins **SGT1** and Rar1 to modulate an innate immune response in plants.

L2 ANSWER 15 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Gene expression profiles of cold-stored and fresh pollen to investigate pollen germination and growth.

=> d bib abs 1 14 11 12

L2 ANSWER 1 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2005:370310 CAPLUS
TI Molecular genetic evidence for the role of **SGT1** in the intramolecular complementation of Bs2 protein activity in Nicotiana benthamiana
AU Leister, R. Todd; Dahlbeck, Douglas; Day, Brad; Li, Yi; Chesnokova, Olga; Staskawicz, Brian J.
CS Department of Plant and Microbial Biology, University of California, Berkeley, CA, 94720-3102, USA
SO Plant Cell (2005), 17(4), 1268-1278
CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Biologists
DT Journal
LA English
AB Pepper plants (Capsicum annuum) containing the Bs2 resistance gene are resistant to strains of Xanthomonas campestris pv vesicatoria (Xcv) expressing the bacterial effector protein AvrBs2. AvrBs2 is delivered directly to the plant cell via the type III protein secretion system (TTSS) of Xcv. Upon recognition of AvrBs2 by plants expressing the Bs2 gene, a signal transduction cascade is activated leading to a bacterial disease resistance response. Here, we describe a novel pathosystem that consists of epitope-tagged Bs2-expressing transgenic Nicotiana benthamiana plants and engineered strains of Pseudomonas syringae pv tabaci that deliver the effector domain of the Xcv AvrBs2 protein via the TTSS of P. syringae. This pathosystem has allowed us to exploit N. benthamiana as a model host plant to use Agrobacterium tumefaciens-mediated transient

protein expression in conjunction with virus-induced gene silencing to validate genes and to identify protein interactions required for the expression of plant host resistance. In this study, we demonstrate that two genes, NbSGT1 and NbNPK1, are required for the Bs2/AvrBs2-mediated resistance responses but that NbRAR1 is not. Protein localization studies in these plants indicate that full-length Bs2 is primarily localized in the plant cytoplasm. Three protein domains of Bs2 have been identified: the N terminus, a central nucleotide binding site, and a C-terminal Leu-rich repeat (LRR). Coimmunopptn. studies demonstrate that sep. epitope-tagged Bs2 domain constructs interact in trans specifically in the plant cell. Coimmunopptn. studies also demonstrate that an NbSGT1-dependent intramol. interaction is required for Bs2 function. Addnl., Bs2 has been shown to associate with **SGT1** via the LRR domain of Bs2. These data suggest a role for **SGT1** in the proper folding of Bs2 or the formation of a Bs2-**SGT1**-containing protein complex that is required for the expression of bacterial disease resistance.

L2 ANSWER 14 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2004:238682 BIOSIS
DN PREV200400239097
TI Molecular chaperone Hsp90 associates with resistance protein N and its signaling proteins **SGT1** and Rar1 to modulate an innate immune response in plants.
AU Liu, Yule; Burch-Smith, Tessa; Schiff, Michael; Feng, Suhua; Dinesh-Kumar, Savithramma P. [Reprint Author]
CS Department of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, CT, 06520, USA
savithramma.dinesh-kumar@yale.edu
SO Journal of Biological Chemistry, (January 16 2004) Vol. 279, No. 3, pp. 2101-2108. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 6 May 2004
Last Updated on STN: 6 May 2004
AB **SGT1** and Rar1 are important signaling components of resistance (R) gene-mediated plant innate immune responses. Here we report that **SGT1** and Rar1 associate with the molecular chaperone Hsp90. In addition, we show that Hsp90 associates with the resistance protein N that confers resistance to tobacco mosaic virus. This suggests that Hsp90-**SGT1**-Rar1 and R proteins might exist in one complex. Suppression of Hsp90 in Nicotiana benthamiana plants shows that it plays an important role in plant growth and development. In addition, Hsp90 suppression in NN plants compromises N-mediated resistance to tobacco mosaic virus. Our results reveal a new role for **SGT1**- and Rar1-associated chaperone machinery in R gene-mediated defense signaling.

L2 ANSWER 11 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2004:457325 BIOSIS
DN PREV200400449338
TI **Sgt1** associates with Hsp90: an initial step of assembly of the core kinetochore complex.
AU Bansal, Parmil K.; Abdulle, Rashid; Kitagawa, Katsumi [Reprint Author]
CS Dept Mol Pharmacol, St Jude Childrens Res Hosp, 332 N Lauderdale St, Memphis, TN, 38105, USA
katsumi.kitagawa@stjude.org
SO Molecular and Cellular Biology, (September 2004) Vol. 24, No. 18, pp. 8069-8079. print.
ISSN: 0270-7306 (ISSN print).
DT Article
LA English
ED Entered STN: 24 Nov 2004
Last Updated on STN: 24 Nov 2004
AB The kinetochore, which consists of DNA sequence elements and structural proteins, is essential for high-fidelity chromosome transmission during cell division. In budding yeast, **Sgt1**, together with Skp1, is

required for assembly of the core kinetochore complex (CBF3) via Ctf13 activation. Formation of the active Ctf13-Skp1 complex also requires Hsp90, a molecular chaperone. We have found that **Sgt1** interacts with Hsp90 in yeast. We also have determined that Skp1 and Hsc82 (a yeast Hsp90 protein) bind to the N-terminal region of **Sgt1** that contains tetratricopeptide repeat motifs. Results of sequence and phenotypic analyses of **sgt1** mutants strongly suggest that the N-terminal region containing the Hsc82-binding and Skp1-binding domains of **Sgt1** is important for the kinetochore function of **Sgt1**. We found that Hsp90's binding to **Sgt1** stimulates the binding of **Sgt1** to Skp1 and that **Sgt1** and Hsp90 stimulate the binding of Skp1 to Ctf13, the F-box core kinetochore protein. Our results strongly suggest that **Sgt1** and Hsp90 function in assembling CBF3 by activating Skp1 and Ctf13.

L2 ANSWER 12 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2005:120954 BIOSIS
DN PREV200500110915
TI RAR1 positively controls steady state levels of barley MLA resistance proteins and enables sufficient MLA6 accumulation for effective resistance.
AU Bieri, Stphane [Reprint Author]; Mauch, Stefan; Shen, Qian-Hua; Peart, Jack; Devoto, Alessandra; Casais, Catarina; Ceron, Francesca; Schulze, Sabine; Steinbiss, Hans-Henning; Shirasu, Ken; Schulze-Lefert, Paul
CS Dept Plant Microbe Interact, Max Planck Inst Zuchtungsforsch, D-50829, Cologne, Germany
bieri@mpiz-koeln.mpg.de
SO Plant Cell, (December 2004) Vol. 16, No. 12, pp. 3480-3495. print.
CODEN: PLCEEW. ISSN: 1040-4651.
DT Article
LA English
ED Entered STN: 23 Mar 2005
Last Updated on STN: 23 Mar 2005
AB The polymorphic barley (Hordeum vulgare) Mla locus harbors allelic race-specific resistance (R) genes to the powdery mildew fungus Blumeria graminis f sp hordei. The highly sequence-related MLA proteins contain an N-terminal coiled-coil structure, a central nucleotide binding (NB) site, a Leu-rich repeat (LRR) region, and a C-terminal non-LRR region. Using transgenic barley lines expressing epitope-tagged MLA1 and MLA6 derivatives driven by native regulatory sequences, we show a reversible and salt concentration-dependent distribution of the intracellular MLA proteins in soluble and membrane-associated pools. A posttranscriptional process directs fourfold greater accumulation of MLA1 over MLA6. Unexpectedly, in rar1 mutant plants that are compromised for MLA6 but not MLA1 resistance, the steady state level of both MLA isoforms is reduced. Furthermore, differential steady state levels of MLA1/MLA6 hybrid proteins correlate with their requirement for RAR1; the RAR1-independent hybrid protein accumulates to higher levels and the RAR1-dependent one to lower levels. Interestingly, yeast two-hybrid studies reveal that the LRR domains of RAR1-independent but not RAR1-dependent MLA isoforms interact with **SGT1**, a RAR1 interacting protein required for the function of many NB-LRR type R proteins. Our findings implicate the existence of a conserved mechanism to reach minimal NB-LRR R protein thresholds that are needed to trigger effective resistance responses.

=> d ti 16-25

L2 ANSWER 16 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Gene expression signatures from three genetically separable resistance gene signaling pathways for downy mildew resistance

L2 ANSWER 17 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Arabidopsis downy mildew resistance gene RPP27 encodes a receptor-like protein similar to CLAVATA2 and tomato Cf-9.

L2 ANSWER 18 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on

TI Signaling requirements and role of salicylic acid in HRT- and rrt-mediated resistance to turnip crinkle virus in Arabidopsis.

L2 ANSWER 19 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI **Sgt1** is required for human kinetochore assembly.

L2 ANSWER 20 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Characterization of Rad6 from a higher plant, rice (Oryza sativa L.) and its interaction with **Sgt1**, a subunit of the SCF ubiquitin ligase complex.

L2 ANSWER 21 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Mammalian CHORD-containing protein 1 is a novel heat shock protein 90-interacting protein

L2 ANSWER 22 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Metabolic compensation of steroidal glycoalkaloid biosynthesis in transgenic potato tubers: using reverse genetics to confirm the in vivo enzyme function of a steroidal alkaloid galactosyltransferase

L2 ANSWER 23 OF 87 CABA COPYRIGHT 2005 CABI on STN
TI Mapping genes of Solanum caripense involved in resistance to Phytophthora infestans, the causal agent of potato late blight.

L2 ANSWER 24 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI A single-amino acid substitution in the sixth leucine-rich repeat of barley MLA6 and MLA13 alleviates dependence on RAR1 for disease resistance signaling.

L2 ANSWER 25 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI Expression of RPS4 in tobacco induces an AvrRps4-independent HR that requires EDS1, **SGT1** and HSP90.

=> d bib abs 16 20 25

L2 ANSWER 16 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:536119 CAPLUS
DN 141:187969
TI Gene expression signatures from three genetically separable resistance gene signaling pathways for downy mildew resistance
AU Eulgem, Thomas; Weigman, Victor J.; Chang, Hur-Song; McDowell, John M.; Holub, Eric B.; Glazebrook, Jane; Zhu, Tong; Dangl, Jeffery L.
CS Department of Biology, University of North Carolina, Chapel Hill, NC, 27599, USA
SO Plant Physiology (2004), 135(2), 1129-1144
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB Resistance gene-dependent disease resistance to pathogenic microorganisms is mediated by genetically separable regulatory pathways. Using the GeneChip Arabidopsis genome array, the authors compared the expression profiles of approx. 8,000 Arabidopsis genes following activation of three RPP genes directed against the pathogenic oomycete Peronospora parasitica. Judicious choice of P. parasitica isolates and loss of resistance plant mutants allowed the authors' to compare the responses controlled by three genetically distinct resistance gene-mediated signaling pathways. The authors found that all three pathways can converge, leading to up-regulation of common sets of target genes. At least two temporal patterns of gene activation are triggered by two of the pathways examined Many genes defined by their early and transient increases in expression encode proteins that execute defense biochem., while genes exhibiting a sustained or delayed expression increase predominantly encode putative signaling proteins. Previously defined and novel sequence motifs were enriched in the promoters of genes coregulated by the local defense-signaling network. These putative promoter elements may operate

downstream from signal convergence points.
RE.CNT 76 THERE ARE 76 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 20 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2004:181696 BIOSIS
DN PREV200400184958
TI Characterization of Rad6 from a higher plant, rice (Oryza sativa L.) and its interaction with **Sgt1**, a subunit of the SCF ubiquitin ligase complex.
AU Yamamoto, Taichi; Mori, Yoko; Ishibashi, Toyotaka; Uchiyama, Yukinobu; Sakaguchi, Norihiro; Furukawa, Tomoyuki; Hashimoto, Junji; Kimura, Seisuke; Sakaguchi, Kengo [Reprint Author]
CS Department of Applied Biological Science, Faculty of Science and Technology, Science University of Tokyo, 2641 Yamazaki, Noda-shi, Chiba-ken, 278-8510, Japan
kengo@rs.noda.sut.ac.jp
SO Biochemical and Biophysical Research Communications, (February 6 2004) Vol. 314, No. 2, pp. 434-439. print.
CODEN: BBRCA9. ISSN: 0006-291X.
DT Article
LA English
ED Entered STN: 7 Apr 2004
Last Updated on STN: 7 Apr 2004
AB We report here the existence of interactions between a ubiquitin-conjugating enzyme, Rad6, from rice, Oryza sativa L. cv. Nipponbare (OsRad6), and **Sgt1** (OsSgt1), a novel subunit of the SCF ubiquitin ligase complex. Rad6 is not only related to post-replicational repair but also to the proteasome system, while **Sgt1** has a function in kinetochore assembly. The relationship between the two is unexpected, but of great interest. The open reading frames of OsRad6 and OsSgt1 encode predicted products of 152 and 367 amino acid residues, respectively, with molecular weights of 17.3 and 40.9 kDa. Two-hybrid and pull-down analyses indicated that OsRad6 binds to OsSgt1, and transcripts of both OsRad6 and OsSgt1 were found to be strongly expressed only in the proliferating tissues such as the shoot apical meristem, suggesting that their expression is cell cycle-dependent. The amount of the Rad6 mRNA in cultured cells increased rapidly after division was halted, and mRNA levels of Rad6 and **Sgt1** were induced by UV- and DNA-damaging agents such as MMS or H2O2. The Rad6 pathway for repair or the proteasome system may thus require **Sgt1** as ubiquitin-conjugating enzyme.

L2 ANSWER 25 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
AN 2005:7708 BIOSIS
DN PREV200500000189
TI Expression of RPS4 in tobacco induces an AvrRps4-independent HR that requires EDS1, **SGT1** and HSP90.
AU Zhang, Yan; Dorey, Stephan; Swiderski, Michal; Jones, Jonathan D. G. [Reprint Author]
CS Sainsbury Lab, John Innes Ctr Plant Sci Res, Colney Lane, Norwich, Norfolk, NR4 7UH, UK
jonathan.jones@sainsbury-laboratory.ac.uk
SO Plant Journal, (October 2004) Vol. 40, No. 2, pp. 213-224. print.
ISSN: 0960-7412 (ISSN print).
DT Article
LA English
ED Entered STN: 16 Dec 2004
Last Updated on STN: 16 Dec 2004
AB The ArabidopsisRPS4 gene belongs to the Toll/interleukin-1 receptor/nucleotide-binding site/leucine-rich repeat (TIR-NB-LRR) class of plant resistance (R) genes. It confers resistance to Pseudomonas syringae carrying the avirulence gene avrRps4. Transient expression of genomic RPS4 driven by the 35S promoter in tobacco leaves induces an AvrRps4-independent hypersensitive response (HR). The same phenotype is seen after expression of a full-length RPS4 cDNA. This indicates that alternative splicing of RPS4 is not involved in this HR. The extent of HR

is correlated with RPS4 protein levels. Deletion analyses of RPS4 domains show the TIR domain is required for the HR phenotype. Mutations in the P-loop motif of the NB domain abolish the HR. Using virus-induced gene silencing, we found that the cell death resulting from RPS4 expression is dependent on the three plant signalling components EDS1, **SGT1** and HSP90. All these data suggest that heterologous expression of an R gene can result in activation of cell death even in the absence of its cognate avirulence product, and provides a system for studying the RPS4 domains required for HR.

=> d ti 26-30

L2 ANSWER 26 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Molecular cloning and characterization of **SGT1**.2, a novel splice variant of Homo sapiens **SGT1**

L2 ANSWER 27 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Functional analysis of proteins essential for plant disease resistance

L2 ANSWER 28 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
TI Molecular regulation of sinapate ester metabolism in Brassica napus: expression of genes, properties of the encoded proteins and correlation of enzyme activities with metabolite accumulation

L2 ANSWER 29 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI The tomato resistance protein Bs4 is a predicted non-nuclear TIR-NB-LRR protein that mediates defense responses to severely truncated derivatives of AvrBs4 and overexpressed AvrBs3.

L2 ANSWER 30 OF 87 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
TI AtCPSF73-II gene encoding an Arabidopsis homolog of CPSF 73 kDa subunit is critical for early embryo development.

=> d bib abs 27

L2 ANSWER 27 OF 87 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:296622 CAPLUS
DN 141:391862
TI Functional analysis of proteins essential for plant disease resistance
AU Takahashi, Akira; Ichimura, Kazuya; Shirasu, Ken
CS Sainsbury Lab., John Innes Centre, UK
SO Shokubutsu Saibo Kogaku Shirizu (2004), 19(Bunshi Reberu kara Mita Shokubutsu no Taibyosei), 96-102
CODEN: SSKSFR
PB Shujunsha
DT Journal; General Review
LA Japanese
AB A review on plant disease resistance associated R gene products RAR1 which is required for Mla-12 resistance in Hordeum vulgare, **SGT1** (suppressor of the G2 allele of skp1), HSP90 of Arabidopsis thaliana, NDR1 (non-race-specific disease resistance), EDS1 (enhanced disease susceptibility), PAD4 (phytoalexin deficient), etc.

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STN INTERNATIONAL SESSION SUSPENDED AT 14:51:41 ON 05 MAY 2005